



1

SEQUENCE LISTING

<110> Kock, Michael
Hoeger, Thomas
Kroeger, Burkhard
Otterbach, Bernd
Lubisch, Wilfried
Lemaire, Hans-Georg

<120> Poly (ADP-ribose) polymerase-gene

<130> 0050/49100

<140> US 09/701,586

<141> 1999-06-04

<150> PCT/EP99/03889

<151> 1999-06-04

<160> 35

<170> PatentIn/WordPerfect

<210> 1

<211> 1843

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (3)...(1715)

<223> product is Poly ADP Ribose Polymerase; from brain tissue

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Pro Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr
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JUL 11 2003

TECH CENTER 1600/2900

C4

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Gln Met Asp Tyr Ala Thr Asn Thr Gln Asp Glu Glu Glu Thr Lys Lys	
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gag gaa tct ctt aaa tct ccc ttg aag cca gag tca cag cta gat ctt	671
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cgg gta cag gag tta ata aag ttg atc tgt aat gtt cag gcc atg gaa	719
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Lys Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys	
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Leu Leu Glu Ala Leu Gly Asp Ile Glu Ile Ala Ile Lys Leu Val Lys	
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Ser Arg Leu Lys Asn Thr Gly Leu Leu Leu Leu Ser Glu Val Ala Leu	
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Gly Gln Cys Asn Glu Leu Leu Glu Ala Asn Pro Lys Ala Glu Gly Leu	
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Leu Lys Val Gln Phe Asn Phe Leu Gln Leu Trp	
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<212> PRT

<213> Homo sapiens

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Lys Met Pro Val Ala Gly Gly Lys Ala Asn Lys Asp Arg Thr Glu Asp
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Lys Gln Asp Glu Ser Val Lys Ala Leu Leu Leu Lys Gly Lys Ala Pro
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Val Asp Pro Glu Cys Thr Ala Lys Val Gly Lys Ala His Val Tyr Cys
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Phe Asn Asn Asn Lys Tyr Tyr Leu Ile Gln Leu Leu Glu Asp Asp Ala
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Gln Arg Asn Phe Ser Val Trp Met Arg Trp Gly Arg Val Gly Lys Met
130 135 140

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Asp Arg Glu Lys Phe Glu Lys Val Pro Gly Lys Tyr Asp Met Leu Gln
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Val Gln Glu Leu Ile Lys Leu Ile Cys Asn Val Gln Ala Met Glu Glu
225 230 235 240

Met Met Met Glu Met Lys Tyr Asn Thr Lys Lys Ala Pro Leu Gly Lys
245 250 255

Leu Thr Val Ala Gln Ile Lys Ala Gly Tyr Gln Ser Leu Lys Lys Ile
 260 265 270
 Glu Asp Cys Ile Arg Ala Gly Gln His Gly Arg Ala Leu Met Glu Ala
 275 280 285
 Cys Asn Glu Phe Tyr Thr Arg Ile Pro His Asp Phe Gly Leu Arg Thr
 290 295 300
 Pro Pro Leu Ile Arg Thr Gln Lys Glu Leu Ser Glu Lys Ile Gln Leu
 305 310 315 320
 Leu Glu Ala Leu Gly Asp Ile Glu Ile Ala Ile Lys Leu Val Lys Thr
 325 330 335
 Glu Leu Gln Ser Pro Glu His Pro Leu Asp Gln His Tyr Arg Asn Leu
 340 345 350
 His Cys Ala Leu Arg Pro Leu Asp His Glu Ser Tyr Glu Phe Lys Val
 355 360 365
 Ile Ser Gln Tyr Leu Gln Ser Thr His Ala Pro Thr His Ser Asp Tyr
 370 375 380
 Thr Met Thr Leu Leu Asp Leu Phe Glu Val Glu Lys Asp Gly Glu Lys
 385 390 395 400
 Glu Ala Phe Arg Glu Asp Leu His Asn Arg Met Leu Leu Trp His Gly
 405 410 415
 Ser Arg Met Ser Asn Trp Val Gly Ile Leu Ser His Gly Leu Arg Ile
 420 425 430
 Ala Pro Pro Glu Ala Pro Ile Thr Gly Tyr Met Phe Gly Lys Gly Ile
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 Tyr Phe Ala Asp Met Ser Ser Lys Ser Ala Asn Tyr Cys Phe Ala Ser
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<210> 3
 <211> 2265
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (242)...(1843)
 <223> product is Poly ADP Ribose Polymerase; from uterus tissue

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tctccctaatt tcacgcctga ggctcatgga gagttgctag acctgggact gccctgggag	180
gcgcacacaa ccaggccggg tggcagccag gacctctccc atgtccctgc ttttcttggc	240
c atg gct cca aag ccg aag ccc tgg gta cag act gag ggc cct gag	286
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65 70 75	
aac aag ttc tac atc atc cag ctg ctc caa gac agc aac cgc ttc ttc	526
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Thr Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys	
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Ile Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu Lys	
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Leu Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser Lys			
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Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser Ser			
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His Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro Pro			
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ccc atc aat tcc cct gag ctt ctg cag gcc aag aag gac atg ctg ctg			1102
Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu Leu			
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Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His Arg			
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Cys Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu Glu			
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Asp Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu Trp			
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Leu Leu Glu Val His Leu	
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<212> PRT

<213> Homo sapiens

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Ala	Glu	Ala 35	Leu	Lys	Ala	Ile	Pro 40	Ala	Glu	Lys	Arg	Ile 45	Ile	Arg	Val
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Lys	Phe	Tyr	Ile	Ile 85	Gln	Leu	Leu	Gln	Asp 90	Ser	Asn	Arg	Phe	Phe 95	Thr
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Ile	Thr	Asn 195	Ile	Phe	Ser	Lys	Glu 200	Met	Phe	Lys	Asn	Thr 205	Met	Ala	Leu
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Ile	Asn	Ser 275	Pro	Glu	Leu	Leu	Gln 280	Ala	Lys	Lys	Asp	Met 285	Leu	Leu	Val
Leu	Ala 290	Asp	Ile	Glu	Leu	Ala 295	Gln	Ala	Leu	Gln	Ala 300	Val	Ser	Glu	Gln

Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln
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 Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro Glu Tyr
 325 330 335
 Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His Arg Cys
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 Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu Glu Asp
 355 360 365
 Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu Trp His
 370 375 380
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 385 390 395 400
 Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala
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 420 425 430
 Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Arg
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 Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro Pro Pro
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 Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp Pro Thr
 465 470 475 480
 Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val Pro Gln
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<210> 5

<211> 2265

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (221)...(1843)

<223> product is Poly ADP Ribose Polymerase; from uterus tissue

<400> 5

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gcgcacacaaa ccaggccggg tggcagccag gacctctccc atg tcc ctg ctt ttc	235
Met Ser Leu Leu Phe	
1 5	
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Leu Ala Met Ala Pro Lys Pro Lys Pro Trp Val Gln Thr Glu Gly Pro	
10 15 20	
gag aag aag aag ggc cgg cag gca gga agg gag gag gac ccc ttc cgc	331
Glu Lys Lys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg	
25 30 35	
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Ser Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala Glu Lys Arg Ile Ile	
40 45 50	
cgc gtg gat cca aca tgt cca ctc agc agc aac ccc ggg acc cag gtg	427
Arg Val Asp Pro Thr Cys Pro Leu Ser Ser Asn Pro Gly Thr Gln Val	
55 60 65	
tat gag gac tac aac tgc acc ctg aac cag acc aac atc gag aac aac	475
Tyr Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr Asn Ile Glu Asn Asn	
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aac aac aag ttc tac atc atc cag ctg ctc caa gac agc aac cgc ttc	523
Asn Asn Lys Phe Tyr Ile Ile Gln Leu Leu Gln Asp Ser Asn Arg Phe	
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ttc acc tgc tgg aac cgc tgg ggc cgt gtg gga gag gtc ggc cag tca	571
Phe Thr Cys Trp Asn Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser	
105 110 115	
aag atc aac cac ttc aca agg cta gaa gat gca aag aag gac ttt gag	619
Lys Ile Asn His Phe Thr Arg Leu Glu Asp Ala Lys Lys Asp Phe Glu	
120 125 130	
aag aaa ttt cgg gaa aag acc aag aac aac tgg gca gag cgg gac cac	667
Lys Lys Phe Arg Glu Lys Thr Lys Asn Asn Trp Ala Glu Arg Asp His	
135 140 145	
ttt gtg tct cac ccg ggc aag tac aca ctt atc gaa gta cag gca gag	715
Phe Val Ser His Pro Gly Lys Tyr Thr Leu Ile Glu Val Gln Ala Glu	
150 155 160 165	
gat gag gcc cag gaa gct gtg gtg aag gtg gac aga ggc cca gtg agg	763
Asp Glu Ala Gln Glu Ala Val Val Lys Val Asp Arg Gly Pro Val Arg	
170 175 180	
act gtg act aag ccg gtg cag ccc tgc tcc ctg gac cca gcc acg cag	811
Thr Val Thr Lys Arg Val Gln Pro Cys Ser Leu Asp Pro Ala Thr Gln	
185 190 195	
aag ctc atc act aac atc ttc agc aag gag atg ttc aag aac acc atg	859
Lys Leu Ile Thr Asn Ile Phe Ser Lys Glu Met Phe Lys Asn Thr Met	
200 205 210	

gcc ctc atg gac ctg gat gtg aag aag atg ccc ctg gga aag ctg agc Ala Leu Met Asp Leu Asp Val Lys Lys Met Pro Leu Gly Lys Leu Ser 215 220 225	907
aag caa cag att gca cgg ggt ttc gag gcc ttg gag gcg ctg gag gag Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu 230 235 240 245	955
gcc ctg aaa ggc ccc acg gat ggt ggc caa agc ctg gag gag ctg tcc Ala Leu Lys Gly Pro Thr Asp Gly Gly Gln Ser Leu Glu Glu Leu Ser 250 255 260	1003
tca cac ttt tac acc gtc atc ccg cac aac ttc ggc cac agc cag ccc Ser His Phe Tyr Thr Val Ile Pro His Asn Phe Gly His Ser Gln Pro 265 270 275	1051
ccg ccc atc aat tcc cct gag ctt ctg cag gcc aag aag gac atg ctg Pro Pro Ile Asn Ser Pro Glu Leu Leu Gln Ala Lys Lys Asp Met Leu 280 285 290	1099
ctg gtg ctg gcg gac atc gag ctg gcc cag gcc ctg cag gca gtc tct Leu Val Leu Ala Asp Ile Glu Leu Ala Gln Ala Leu Gln Ala Val Ser 295 300 305	1147
gag cag gag aag acg gtg gag gag gtg cca cac ccc ctg gac cga gac Glu Gln Glu Lys Thr Val Glu Glu Val Pro His Pro Leu Asp Arg Asp 310 315 320 325	1195
tac cag ctt ctg aag tgc cag ctg cag ctg cta gac tct gga gca cct Tyr Gln Leu Leu Lys Cys Gln Leu Gln Leu Leu Asp Ser Gly Ala Pro 330 335 340	1243
gag tac aag gtg ata cag acc tac tta gaa cag act ggc agc aac cac Glu Tyr Lys Val Ile Gln Thr Tyr Leu Glu Gln Thr Gly Ser Asn His 345 350 355	1291
agg tgc cct aca ctt caa cac atc tgg aaa gta aac caa gaa ggg gag Arg Cys Pro Thr Leu Gln His Ile Trp Lys Val Asn Gln Glu Gly Glu 360 365 370	1339
gaa gac aga ttc cag gcc cac tcc aaa ctg ggt aat cgg aag ctg ctg Glu Asp Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Lys Leu Leu 375 380 385	1387
tgg cat ggc acc aac atg gcc gtg gtg gcc gcc atc ctg act agt ggg Trp His Gly Thr Asn Met Ala Val Val Ala Ala Ile Leu Thr Ser Gly 390 395 400 405	1435
ctc cgc atc atg cca cat tct ggt ggg cgt gtt ggc aag ggc atc tac Leu Arg Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr 410 415 420	1483
ttt gcc tca gag aac agc aag tca gct gga tat gtt att ggc atg aag Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Ile Gly Met Lys 425 430 435	1531
tgt ggg gcc cac cat gtc ggc tac atg ttc ctg ggt gag gtg gcc ctg Cys Gly Ala His His Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu 440 445 450	1579

ggc aga gag cac cat atc aac acg gac aac ccc agc ttg aag agc cca 1627
 Gly Arg Glu His His Ile Asn Thr Asp Asn Pro Ser Leu Lys Ser Pro
 455 460 465

 cct cct ggc ttc gac agt gtc att gcc cga ggc cac acc gag cct gat 1675
 Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly His Thr Glu Pro Asp
 470 475 480 485

 ccg acc cag gac act gag ttg gag ctg gat ggc cag caa gtg gtg gtg 1723
 Pro Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly Gln Gln Val Val Val
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 ccc cag ggc cag cct gtg ccc tgc cca gag ttc agc agc tcc aca ttc 1771
 Pro Gln Gly Gln Pro Val Pro Cys Pro Glu Phe Ser Ser Thr Phe
 505 510 515

 tcc cag agc gag tac ctc atc tac cag gag agc cag tgt cgc ctg cgc 1819
 Ser Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser Gln Cys Arg Leu Arg
 520 525 530

 tac ctg ctg gag gtc cac ctc tga gtgccccgcc tgtcccccg ggtcctgcaa 1873
 Tyr Leu Leu Glu Val His Leu
 535 540

 ggctggactg tgatcttcaa tcatcctgcc catctctggt acccctatat cactcctttt 1933
 tttcaagaat acaatacggt gttgttaact atagtcacca tgctgtacaa gatccctgaa 1993
 cttatgcctc ctaactgaaa ttttgtattc tttgacacat ctgcccagtc cctctcctcc 2053
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 aaaaaaaaa aaaaaaaaa aaaaaaaaa aa 2265

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 <212> PRT
 <213> Homo sapiens

<400> 6

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 Glu Asp Pro Phe Arg Ser Thr Ala Glu Ala Leu Lys Ala Ile Pro Ala
 35 40 45
 Glu Lys Arg Ile Ile Arg Val Asp Pro Thr Cys Pro Leu Ser Ser Asn
 50 55 60
 Pro Gly Thr Gln Val Tyr Glu Asp Tyr Asn Cys Thr Leu Asn Gln Thr

65					70						75				80
Asn	Ile	Glu	Asn	Asn	Asn	Asn	Lys	Phe	Tyr	Ile	Ile	Gln	Leu	Leu	Gln
				85					90					95	
Asp	Ser	Asn	Arg	Phe	Phe	Thr	Cys	Trp	Asn	Arg	Trp	Gly	Arg	Val	Gly
			100					105					110		
Glu	Val	Gly	Gln	Ser	Lys	Ile	Asn	His	Phe	Thr	Arg	Leu	Glu	Asp	Ala
		115					120					125			
Lys	Lys	Asp	Phe	Glu	Lys	Lys	Phe	Arg	Glu	Lys	Thr	Lys	Asn	Asn	Trp
	130					135					140				
Ala	Glu	Arg	Asp	His	Phe	Val	Ser	His	Pro	Gly	Lys	Tyr	Thr	Leu	Ile
145					150					155					160
Glu	Val	Gln	Ala	Glu	Asp	Glu	Ala	Gln	Glu	Ala	Val	Val	Lys	Val	Asp
				165					170					175	
Arg	Gly	Pro	Val	Arg	Thr	Val	Thr	Lys	Arg	Val	Gln	Pro	Cys	Ser	Leu
			180					185					190		
Asp	Pro	Ala	Thr	Gln	Lys	Leu	Ile	Thr	Asn	Ile	Phe	Ser	Lys	Glu	Met
		195					200					205			
Phe	Lys	Asn	Thr	Met	Ala	Leu	Met	Asp	Leu	Asp	Val	Lys	Lys	Met	Pro
	210					215					220				
Leu	Gly	Lys	Leu	Ser	Lys	Gln	Gln	Ile	Ala	Arg	Gly	Phe	Glu	Ala	Leu
225					230					235					240
Glu	Ala	Leu	Glu	Glu	Ala	Leu	Lys	Gly	Pro	Thr	Asp	Gly	Gly	Gln	Ser
				245					250					255	
Leu	Glu	Glu	Leu	Ser	Ser	His	Phe	Tyr	Thr	Val	Ile	Pro	His	Asn	Phe
			260					265					270		
Gly	His	Ser	Gln	Pro	Pro	Pro	Ile	Asn	Ser	Pro	Glu	Leu	Leu	Gln	Ala
		275					280					285			
Lys	Lys	Asp	Met	Leu	Leu	Val	Leu	Ala	Asp	Ile	Glu	Leu	Ala	Gln	Ala
	290					295					300				
Leu	Gln	Ala	Val	Ser	Glu	Gln	Glu	Lys	Thr	Val	Glu	Glu	Val	Pro	His
305					310					315				320	
Pro	Leu	Asp	Arg	Asp	Tyr	Gln	Leu	Leu	Lys	Cys	Gln	Leu	Gln	Leu	Leu
				325					330					335	
Asp	Ser	Gly	Ala	Pro	Glu	Tyr	Lys	Val	Ile	Gln	Thr	Tyr	Leu	Glu	Gln
			340					345					350		
Thr	Gly	Ser	Asn	His	Arg	Cys	Pro	Thr	Leu	Gln	His	Ile	Trp	Lys	Val
		355					360					365			
Asn	Gln	Glu	Gly	Glu	Glu	Asp	Arg	Phe	Gln	Ala	His	Ser	Lys	Leu	Gly
	370					375					380				

Asn Arg Lys Leu Leu Trp His Gly Thr Asn Met Ala Val Val Ala Ala
 385 390 395 400
 Ile Leu Thr Ser Gly Leu Arg Ile Met Pro His Ser Gly Gly Arg Val
 405 410 415
 Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly Tyr
 420 425 430
 Val Ile Gly Met Lys Cys Gly Ala His His Val Gly Tyr Met Phe Leu
 435 440 445
 Gly Glu Val Ala Leu Gly Arg Glu His His Ile Asn Thr Asp Asn Pro
 450 455 460
 Ser Leu Lys Ser Pro Pro Gly Phe Asp Ser Val Ile Ala Arg Gly
 465 470 475 480
 His Thr Glu Pro Asp Pro Thr Gln Asp Thr Glu Leu Glu Leu Asp Gly
 485 490 495
 Gln Gln Val Val Val Pro Gln Gly Gln Pro Val Pro Cys Pro Glu Phe
 500 505 510
 Ser Ser Ser Thr Phe Ser Gln Ser Glu Tyr Leu Ile Tyr Gln Glu Ser
 515 520 525
 Gln Cys Arg Leu Arg Tyr Leu Leu Glu Val His Leu
 530 535 540

<210> 7

<211> 1740

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (112)...(1710)

<400> 7

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 Met Ala
 1
 cca aaa cga aag gcc tct gtg cag act gag ggc tcc aag aag cag cga 165
 Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys Gln Arg
 5 10 15
 caa ggg aca gag gag gag gac agc ttc cgg tcc act gcc gag gct ctc 213
 Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu Ala Leu
 20 25 30
 aga gca gca cct gct gat aat cgg gtc atc cgt gtg gac ccc tca tgt 261
 Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro Ser Cys
 35 40 45 50

cca ttc agc cgg aac ccc ggg ata cag gtc cac gag gac tat gac tgt	309
Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr Asp Cys	
55 60 65	
acc ctg aac cag acc aac atc ggc aac aac aac aac aag ttc tat att	357
Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe Tyr Ile	
70 75 80	
atc caa ctg ctg gag gag ggt agt cgc ttc ttc tgc tgg aat cgc tgg	405
Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn Arg Trp	
85 90 95	
ggc cgc gtg gga gag gtg ggc cag agc aag atg aac cac ttc acc tgc	453
Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe Thr Cys	
100 105 110	
ctg gaa gat gca aag aag gac ttt aag aag aaa ttt tgg gag aag act	501
Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu Lys Thr	
115 120 125 130	
aaa aac aaa tgg gag gag cgg gac cgt ttt gtg gcc cag ccc aac aag	549
Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro Asn Lys	
135 140 145	
tac aca ctt ata gaa gtc cag gga gaa gca gag agc caa gag gct gta	597
Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu Ala Val	
150 155 160	
gtg aag gcc tta tct ccc cag gtg gac agc ggc cct gtg agg acc gtg	645
Val Lys Ala Leu Ser Pro Gln Val Asp Ser Gly Pro Val Arg Thr Val	
165 170 175	
gtc aag ccc tgc tcc cta gac cct gcc acc cag aac ctt atc acc aac	693
Val Lys Pro Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn	
180 185 190	
atc ttc agc aaa gag atg ttc aag aac gca atg acc ctc atg aac ctg	741
Ile Phe Ser Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu	
195 200 205 210	
gat gtg aag aag atg ccc ttg gga aag ctg acc aag cag cag att gcc	789
Asp Val Lys Lys Met Pro Leu Gly Lys Leu Thr Lys Gln Gln Ile Ala	
215 220 225	
cgt ggc ttc gag gcc ttg gaa gct cta gag gag gcc atg aaa aac ccc	837
Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu Ala Met Lys Asn Pro	
230 235 240	
aca ggg gat ggc cag agc ctg gaa gag ctc tcc tcc tgc ttc tac act	885
Thr Gly Asp Gly Gln Ser Leu Glu Glu Leu Ser Ser Cys Phe Tyr Thr	
245 250 255	
gtc atc cca cac aac ttc ggc cgc agc cga ccc ccg ccc atc aac tcc	933
Val Ile Pro His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile Asn Ser	
260 265 270	
cct gat gtg ctt cag gcc aag aag gac atg ctg ctg gtg cta gcg gac	981
Pro Asp Val Leu Gln Ala Lys Lys Asp Met Leu Val Leu Ala Asp	
275 280 285 290	

atc gag ttg gcg cag acc ttg cag gca gcc cct ggg gag gag gag gag	1029
Ile Glu Leu Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu Glu Glu	
295 300 305	
aaa gtg gaa gag gtg cca cac cca ctg gat cga gac tac cag ctc ctc	1077
Lys Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln Leu Leu	
310 315 320	
agg tgc cag ctt caa ctg ctg gac tcc ggg gag tcc gag tac aag gca	1125
Arg Cys Gln Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr Lys Ala	
325 330 335	
ata cag acc tac ctg aaa cag act ggc aac agc tac agg tgc cca aac	1173
Ile Gln Thr Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys Pro Asn	
340 345 350	
ctg cgg cat gtt tgg aaa gtg aac cga gaa ggg gag gga gac agg ttc	1221
Leu Arg His Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp Arg Phe	
355 360 365 370	
cag gcc cac tcc aaa ctg ggc aat cgg agg ctg ctg tgg cac ggc acc	1269
Gln Ala His Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His Gly Thr	
375 380 385	
aat gtg gcc gtg gtg gct gcc atc ctc acc agt ggg ctc cga atc atg	1317
Asn Val Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg Ile Met	
390 395 400	
cca cac tcg ggt ggt cgt gtt ggc aag ggt att tat ttt gcc tct gag	1365
Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu	
405 410 415	
aac agc aag tca gct ggc tat gtt acc acc atg cac tgt ggg ggc cac	1413
Asn Ser Lys Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly Gly His	
420 425 430	
cag gtg ggc tac atg ttc ctg ggc gag gtg gcc ctc ggc aaa gag cac	1461
Gln Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys Glu His	
435 440 445 450	
cac atc acc atc gat gac ccc agc ttg aag agt cca ccc cct ggc ttt	1509
His Ile Thr Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe	
455 460 465	
gac agc gtc atc gcc cga ggc caa acc gag ccg gat ccc gcc cag gac	1557
Asp Ser Val Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp	
470 475 480	
att gaa ctt gaa ctg gat ggg cag ccg gtg gtg gtg ccc caa ggc ccg	1605
Ile Glu Leu Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro	
485 490 495	
cct gtg cag tgc ccg tca ttc aaa agc tcc agc ttc agc cag agt gaa	1653
Pro Val Gln Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu	
500 505 510	
tac ctc ata tac aag gag agc cag tgt cgc ctg cgc tac ctg ctg gag	1701
Tyr Leu Ile Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu	
515 520 525 530	

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Ile His Leu

1740

<210> 8
<211> 533
<212> PRT
<213> Mus musculus

<400> 8

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Gln	Arg	Gln	Gly	Thr	Glu	Glu	Glu	Asp	Ser	Phe	Arg	Ser	Thr	Ala	Glu	20	25	30	
Ala	Leu	Arg	Ala	Ala	Pro	Ala	Asp	Asn	Arg	Val	Ile	Arg	Val	Asp	Pro	35	40	45	
Ser	Cys	Pro	Phe	Ser	Arg	Asn	Pro	Gly	Ile	Gln	Val	His	Glu	Asp	Tyr	50	55	60	
Asp	Cys	Thr	Leu	Asn	Gln	Thr	Asn	Ile	Gly	Asn	Asn	Asn	Asn	Lys	Phe	65	70	75	80
Tyr	Ile	Ile	Gln	Leu	Leu	Glu	Glu	Gly	Ser	Arg	Phe	Phe	Cys	Trp	Asn	85	90	95	
Arg	Trp	Gly	Arg	Val	Gly	Glu	Val	Gly	Gln	Ser	Lys	Met	Asn	His	Phe	100	105	110	
Thr	Cys	Leu	Glu	Asp	Ala	Lys	Lys	Asp	Phe	Lys	Lys	Lys	Phe	Trp	Glu	115	120	125	
Lys	Thr	Lys	Asn	Lys	Trp	Glu	Glu	Arg	Asp	Arg	Phe	Val	Ala	Gln	Pro	130	135	140	
Asn	Lys	Tyr	Thr	Leu	Ile	Glu	Val	Gln	Gly	Glu	Ala	Glu	Ser	Gln	Glu	145	150	155	160
Ala	Val	Val	Lys	Ala	Leu	Ser	Pro	Gln	Val	Asp	Ser	Gly	Pro	Val	Arg	165	170	175	
Thr	Val	Val	Lys	Pro	Cys	Ser	Leu	Asp	Pro	Ala	Thr	Gln	Asn	Leu	Ile	180	185	190	
Thr	Asn	Ile	Phe	Ser	Lys	Glu	Met	Phe	Lys	Asn	Ala	Met	Thr	Leu	Met	195	200	205	
Asn	Leu	Asp	Val	Lys	Lys	Met	Pro	Leu	Gly	Lys	Leu	Thr	Lys	Gln	Gln	210	215	220	
Ile	Ala	Arg	Gly	Phe	Glu	Ala	Leu	Glu	Ala	Leu	Glu	Glu	Ala	Met	Lys	225	230	235	240
Asn	Pro	Thr	Gly	Asp	Gly	Gln	Ser	Leu	Glu	Glu	Leu	Ser	Ser	Cys	Phe	245	250	255	

Tyr Thr Val Ile Pro His Asn Phe Gly Arg Ser Arg Pro Pro Pro Ile
 260 265 270
 Asn Ser Pro Asp Val Leu Gln Ala Lys Lys Asp Met Leu Leu Val Leu
 275 280 285
 Ala Asp Ile Glu Leu Ala Gln Thr Leu Gln Ala Ala Pro Gly Glu Glu
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 Glu Glu Lys Val Glu Glu Val Pro His Pro Leu Asp Arg Asp Tyr Gln
 305 310 315 320
 Leu Leu Arg Cys Gln Leu Gln Leu Leu Asp Ser Gly Glu Ser Glu Tyr
 325 330 335
 Lys Ala Ile Gln Thr Tyr Leu Lys Gln Thr Gly Asn Ser Tyr Arg Cys
 340 345 350
 Pro Asn Leu Arg His Val Trp Lys Val Asn Arg Glu Gly Glu Gly Asp
 355 360 365
 Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg Arg Leu Leu Trp His
 370 375 380
 Gly Thr Asn Val Ala Val Val Ala Ala Ile Leu Thr Ser Gly Leu Arg
 385 390 395 400
 Ile Met Pro His Ser Gly Gly Arg Val Gly Lys Gly Ile Tyr Phe Ala
 405 410 415
 Ser Glu Asn Ser Lys Ser Ala Gly Tyr Val Thr Thr Met His Cys Gly
 420 425 430
 Gly His Gln Val Gly Tyr Met Phe Leu Gly Glu Val Ala Leu Gly Lys
 435 440 445
 Glu His His Ile Thr Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro
 450 455 460
 Gly Phe Asp Ser Val Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala
 465 470 475 480
 Gln Asp Ile Glu Leu Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln
 485 490 495
 Gly Pro Pro Val Gln Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln
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 Leu Glu Ile His Leu
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<211> 1587

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)...(1584)

<400> 9

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cag cga caa ggg aca gag gag gag gac agc ttc cgg tcc act gcc gag	96
Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu	
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gct ctc aga gca gca cct gct gat aat cgg gtc atc cgt gtg gac ccc	144
Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro	
35 40 45	
tca tgt cca ttc agc cgg aac ccc ggg ata cag gtc cac gag gac tat	192
Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr	
50 55 60	
gac tgt acc ctg aac cag acc aac atc ggc aac aac aac aac aag ttc	240
Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe	
65 70 75 80	
tat att atc caa ctg ctg gag gag ggt agt cgc ttc ttc tgc tgg aat	288
Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn	
85 90 95	
cgc tgg ggc cgc gtg gga gag gtg ggc cag agc aag atg aac cac ttc	336
Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe	
100 105 110	
acc tgc ctg gaa gat gca aag aag gac ttt aag aag aaa ttt tgg gag	384
Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu	
115 120 125	
aag act aaa aac aaa tgg gag gag cgg gac cgt ttt gtg gcc cag ccc	432
Lys Thr Lys Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro	
130 135 140	
aac aag tac aca ctt ata gaa gtc cag gga gaa gca gag agc caa gag	480
Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu	
145 150 155 160	
gct gta gtg aag gtg gac agc ggc cct gtg agg acc gtg gtc aag ccc	528
Ala Val Val Lys Val Asp Ser Gly Pro Val Arg Thr Val Val Lys Pro	
165 170 175	
tgc tcc cta gac cct gcc acc cag aac ctt atc acc aac atc ttc agc	576
Cys Ser Leu Asp Pro Ala Thr Gln Asn Leu Ile Thr Asn Ile Phe Ser	
180 185 190	
aaa gag atg ttc aag aac gca atg acc ctc atg aac ctg gat gtg aag	624
Lys Glu Met Phe Lys Asn Ala Met Thr Leu Met Asn Leu Asp Val Lys	
195 200 205	
aag atg ccc ttg gga aag ctg acc aag cag cag att gcc cgt ggc ttc	672

Lys	Met	Pro	Leu	Gly	Lys	Leu	Thr	Lys	Gln	Gln	Ile	Ala	Arg	Gly	Phe	
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gag	gcc	ttg	gaa	gct	cta	gag	gag	gcc	atg	aaa	aac	ccc	aca	ggg	gat	720
Glu	Ala	Leu	Glu	Ala	Leu	Glu	Glu	Ala	Met	Lys	Asn	Pro	Thr	Gly	Asp	
225					230					235					240	
ggc	cag	agc	ctg	gaa	gag	ctc	tcc	tcc	tgc	ttc	tac	act	gtc	atc	cca	768
Gly	Gln	Ser	Leu	Glu	Glu	Leu	Ser	Ser	Cys	Phe	Tyr	Thr	Val	Ile	Pro	
			245						250					255		
cac	aac	ttc	ggc	cgc	agc	cga	ccc	ccg	ccc	atc	aac	tcc	cct	gat	gtg	816
His	Asn	Phe	Gly	Arg	Ser	Arg	Pro	Pro	Pro	Ile	Asn	Ser	Pro	Asp	Val	
			260					265					270			
ctt	cag	gcc	aag	aag	gac	atg	ctg	ctg	gtg	cta	gcg	gac	atc	gag	ttg	864
Leu	Gln	Ala	Lys	Lys	Asp	Met	Leu	Leu	Val	Leu	Ala	Asp	Ile	Glu	Leu	
		275					280					285				
gcg	cag	acc	ttg	cag	gca	gcc	cct	ggg	gag	gag	gag	gag	aaa	gtg	gaa	912
Ala	Gln	Thr	Leu	Gln	Ala	Ala	Pro	Gly	Glu	Glu	Glu	Glu	Lys	Val	Glu	
	290					295					300					
gag	gtg	cca	cac	cca	ctg	gat	cga	gac	tac	cag	ctc	ctc	agg	tgc	cag	960
Glu	Val	Pro	His	Pro	Leu	Asp	Arg	Asp	Tyr	Gln	Leu	Leu	Arg	Cys	Gln	
305					310					315					320	
ctt	caa	ctg	ctg	gac	tcc	ggg	gag	tcc	gag	tac	aag	gca	ata	cag	acc	1008
Leu	Gln	Leu	Leu	Asp	Ser	Gly	Glu	Ser	Glu	Tyr	Lys	Ala	Ile	Gln	Thr	
				325					330					335		
tac	ctg	aaa	cag	act	ggc	aac	agc	tac	agg	tgc	cca	aac	ctg	cgg	cat	1056
Tyr	Leu	Lys	Gln	Thr	Gly	Asn	Ser	Tyr	Arg	Cys	Pro	Asn	Leu	Arg	His	
			340					345					350			
gtt	tgg	aaa	gtg	aac	cga	gaa	ggg	gag	gga	gac	agg	ttc	cag	gcc	cac	1104
Val	Trp	Lys	Val	Asn	Arg	Glu	Gly	Glu	Gly	Asp	Arg	Phe	Gln	Ala	His	
	355						360					365				
tcc	aaa	ctg	ggc	aat	cgg	agg	ctg	ctg	tgg	cac	ggc	acc	aat	gtg	gcc	1152
Ser	Lys	Leu	Gly	Asn	Arg	Arg	Leu	Leu	Trp	His	Gly	Thr	Asn	Val	Ala	
	370					375					380					
gtg	gtg	gct	gcc	atc	ctc	acc	agt	ggg	ctc	cga	atc	atg	cca	cac	tcg	1200
Val	Val	Ala	Ala	Ile	Leu	Thr	Ser	Gly	Leu	Arg	Ile	Met	Pro	His	Ser	
385					390				395						400	
ggt	ggt	cgt	gtt	ggc	aag	ggt	att	tat	ttt	gcc	tct	gag	aac	agc	aag	1248
Gly	Gly	Arg	Val	Gly	Lys	Gly	Ile	Tyr	Phe	Ala	Ser	Glu	Asn	Ser	Lys	
			405						410					415		
tca	gct	ggc	tat	gtt	acc	acc	atg	cac	tgt	ggg	ggc	cac	cag	gtg	ggc	1296
Ser	Ala	Gly	Tyr	Val	Thr	Thr	Met	His	Cys	Gly	Gly	His	Gln	Val	Gly	
			420					425					430			
tac	atg	ttc	ctg	ggc	gag	gtg	gcc	ctc	ggc	aaa	gag	cac	cac	atc	acc	1344
Tyr	Met	Phe	Leu	Gly	Glu	Val	Ala	Leu	Gly	Lys	Glu	His	His	Ile	Thr	
	435					440					445					

atc gat gac ccc agc ttg aag agt cca ccc cct ggc ttt gac agc gtc 1392
 Ile Asp Asp Pro Ser Leu Lys Ser Pro Pro Pro Gly Phe Asp Ser Val
 450 455 460

atc gcc cga ggc caa acc gag ccg gat ccc gcc cag gac att gaa ctt 1440
 Ile Ala Arg Gly Gln Thr Glu Pro Asp Pro Ala Gln Asp Ile Glu Leu
 465 470 475 480

gaa ctg gat ggg cag ccg gtg gtg gtg ccc caa ggc ccg cct gtg cag 1488
 Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro Pro Val Gln
 485 490 495

tgc ccg tca ttc aaa agc tcc agc ttc agc cag agt gaa tac ctc ata 1536
 Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu Tyr Leu Ile
 500 505 510

tac aag gag agc cag tgt cgc ctg cgc tac ctg ctg gag att cac ctc 1584
 Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu Ile His Leu
 515 520 525

taa 1587

<210> 10
 <211> 528
 <212> PRT
 <213> Mus musculus

<400> 10

Met Ala Pro Lys Arg Lys Ala Ser Val Gln Thr Glu Gly Ser Lys Lys
 1 5 10 15

Gln Arg Gln Gly Thr Glu Glu Glu Asp Ser Phe Arg Ser Thr Ala Glu
 20 25 30

Ala Leu Arg Ala Ala Pro Ala Asp Asn Arg Val Ile Arg Val Asp Pro
 35 40 45

Ser Cys Pro Phe Ser Arg Asn Pro Gly Ile Gln Val His Glu Asp Tyr
 50 55 60

Asp Cys Thr Leu Asn Gln Thr Asn Ile Gly Asn Asn Asn Asn Lys Phe
 65 70 75 80

Tyr Ile Ile Gln Leu Leu Glu Glu Gly Ser Arg Phe Phe Cys Trp Asn
 85 90 95

Arg Trp Gly Arg Val Gly Glu Val Gly Gln Ser Lys Met Asn His Phe
 100 105 110

Thr Cys Leu Glu Asp Ala Lys Lys Asp Phe Lys Lys Lys Phe Trp Glu
 115 120 125

Lys Thr Lys Asn Lys Trp Glu Glu Arg Asp Arg Phe Val Ala Gln Pro
 130 135 140

Asn Lys Tyr Thr Leu Ile Glu Val Gln Gly Glu Ala Glu Ser Gln Glu
 145 150 155 160

Ala	Val	Val	Lys	Val	Asp	Ser	Gly	Pro	Val	Arg	Thr	Val	Val	Lys	Pro	165	170	175
Cys	Ser	Leu	Asp	Pro	Ala	Thr	Gln	Asn	Leu	Ile	Thr	Asn	Ile	Phe	Ser	180	185	190
Lys	Glu	Met	Phe	Lys	Asn	Ala	Met	Thr	Leu	Met	Asn	Leu	Asp	Val	Lys	195	200	205
Lys	Met	Pro	Leu	Gly	Lys	Leu	Thr	Lys	Gln	Gln	Ile	Ala	Arg	Gly	Phe	210	215	220
Glu	Ala	Leu	Glu	Ala	Leu	Glu	Glu	Ala	Met	Lys	Asn	Pro	Thr	Gly	Asp	225	230	235
Gly	Gln	Ser	Leu	Glu	Glu	Leu	Ser	Ser	Cys	Phe	Tyr	Thr	Val	Ile	Pro	245	250	255
His	Asn	Phe	Gly	Arg	Ser	Arg	Pro	Pro	Pro	Ile	Asn	Ser	Pro	Asp	Val	260	265	270
Leu	Gln	Ala	Lys	Lys	Asp	Met	Leu	Leu	Val	Leu	Ala	Asp	Ile	Glu	Leu	275	280	285
Ala	Gln	Thr	Leu	Gln	Ala	Ala	Pro	Gly	Glu	Glu	Glu	Glu	Lys	Val	Glu	290	295	300
Glu	Val	Pro	His	Pro	Leu	Asp	Arg	Asp	Tyr	Gln	Leu	Leu	Arg	Cys	Gln	305	310	315
Leu	Gln	Leu	Leu	Asp	Ser	Gly	Glu	Ser	Glu	Tyr	Lys	Ala	Ile	Gln	Thr	325	330	335
Tyr	Leu	Lys	Gln	Thr	Gly	Asn	Ser	Tyr	Arg	Cys	Pro	Asn	Leu	Arg	His	340	345	350
Val	Trp	Lys	Val	Asn	Arg	Glu	Gly	Glu	Gly	Asp	Arg	Phe	Gln	Ala	His	355	360	365
Ser	Lys	Leu	Gly	Asn	Arg	Arg	Leu	Leu	Trp	His	Gly	Thr	Asn	Val	Ala	370	375	380
Val	Val	Ala	Ala	Ile	Leu	Thr	Ser	Gly	Leu	Arg	Ile	Met	Pro	His	Ser	385	390	395
Gly	Gly	Arg	Val	Gly	Lys	Gly	Ile	Tyr	Phe	Ala	Ser	Glu	Asn	Ser	Lys	405	410	415
Ser	Ala	Gly	Tyr	Val	Thr	Thr	Met	His	Cys	Gly	Gly	His	Gln	Val	Gly	420	425	430
Tyr	Met	Phe	Leu	Gly	Glu	Val	Ala	Leu	Gly	Lys	Glu	His	His	Ile	Thr	435	440	445
Ile	Asp	Asp	Pro	Ser	Leu	Lys	Ser	Pro	Pro	Pro	Gly	Phe	Asp	Ser	Val	450	455	460
Ile	Ala	Arg	Gly	Gln	Thr	Glu	Pro	Asp	Pro	Ala	Gln	Asp	Ile	Glu	Leu	465	470	475

Glu Leu Asp Gly Gln Pro Val Val Val Pro Gln Gly Pro Pro Val Gln
 485 490 495

Cys Pro Ser Phe Lys Ser Ser Ser Phe Ser Gln Ser Glu Tyr Leu Ile
 500 505 510

Tyr Lys Glu Ser Gln Cys Arg Leu Arg Tyr Leu Leu Glu Ile His Leu
 515 520 525

<210> 11
 <211> 18
 <212> PRT
 <213> artificial sequence

<220>
 <223> NAD+ binding domain

<220>
 <221> VARIANT
 <222> (2)...(6), (9)...(11)
 <223> any amino acid; residues 3 to 6 may be present or absent

<220>
 <221> VARIANT
 <222> (7)
 <223> amino acid residue 7 is either Ser or Thr

<400> 11

Pro Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Gly Lys Gly Ile Tyr
 1 5 10 15

Phe Ala

<210> 12
 <211> 25
 <212> PRT
 <213> artificial sequence

<220>
 <223> NAD+ binding domain

<220>
 <221> VARIANT
 <222> (1), (14)
 <223> amino acid residues 1 and 14 are either Ser or Thr

<220>
 <221> VARIANT
 <222> (2), (7), (9)...(13), (16)...(18)
 <223> may be any amino acid; 10-13 may be present or absent

<220>
 <221> VARIANT
 <222> (6)
 <223> amino acid residue 6 is either Ile or Val

<400> 12

Xaa Xaa Gly Leu Arg Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa
 1 5 10 15

Xaa Xaa Gly Lys Gly Ile Tyr Phe Ala
 20 25

<210> 13

<211> 49

<212> PRT

<213> artificial sequence

<220>

<223> NAD+ binding domain

<220>

<221> VARIANT

<222> (6), (16), (29)

<223> Ser or Thr

<220>

<221> VARIANT

<222> (7)...(13), (17), (22), (24)...(28), (31)...(33), (41)...(43), (48)

<223> may be any amino acid; residues 25-28 may be present or absent

<220>

<221> VARIANT

<222> 21

<223> Ile or Val

<400> 13

Leu Leu Trp His Gly Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Ile Leu Xaa
 1 5 10 15

Xaa Gly Leu Arg Xaa Xaa Pro Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa
 20 25 30

Xaa Gly Lys Gly Ile Tyr Phe Ala Xaa Xaa Xaa Ser Lys Ser Ala Xaa
 35 40 45

Tyr

<210> 14

<211> 22

<212> PRT

<213> artificial sequence

<220>

<223> leucine zipper motif

<220>

<221> VARIANT

<222> (1)

<223> Leu or Val

<220>
 <221> VARIANT
 <222> (2)...(7), (9)...(14), (16)...(21)
 <223> may be any amino acid

<400> 14

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Leu
 20

<210> 15
 <211> 37
 <212> PRT
 <213> artificial sequence

<220>
 <223> part-sequence motif 1

<220>
 <221> VARIANT
 <222> (21)
 <223> Asp or Glu

<220>
 <221> VARIANT
 <222> (2)...(10), (12)...(13), (15)...(16), (20), (22)...(32)
 <223> may be any amino acid; residue 32 may be present or absent

<400> 15

Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Asn Xaa Xaa Tyr Xaa Xaa
 1 5 10 15

Gln Leu Leu Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30

Trp Gly Arg Val Gly
 35

<210> 16
 <211> 29
 <212> PRT
 <213> artificial sequence

<220>
 <223> part-sequence motif 2

<220>
 <221> VARIANT
 <222> (2)...(4), (6), (8)...(11), (14), (16), (18)...(22), (24)...(26), (28)
 <223> may be any amino acid

<400> 16

Ala Xaa Xaa Xaa Phe Xaa Lys Xaa Xaa Xaa Xaa Lys Thr Xaa Asn Xaa
 1 5 10 15

Trp Xaa Xaa Xaa Xaa Xaa Phe Xaa Xaa Xaa Pro Xaa Lys
 20 25

<210> 17
 <211> 44
 <212> PRT
 <213> artificial sequence

<220>
 <223> part-sequence motif 3

<220>
 <221> VARIANT
 <222> (2), (5)...(6), (8)...(16), (18)...(27), (33)...(35), (38)...(43)
 <223> may be any amino acid

<220>
 <221> VARIANT
 <222> (4)
 <223> Ile or Leu

<400> 17

Gln Xaa Leu Xaa Xaa Xaa Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

Met Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Pro Leu Gly Lys Leu
 20 25 30

Xaa Xaa Xaa Gln Ile Xaa Xaa Xaa Xaa Xaa Xaa Xaa Leu
 35 40

<210> 18
 <211> 15
 <212> PRT
 <213> artificial sequence

<220>
 <223> part-sequence motif 4

<220>
 <221> VARIANT
 <222> (4), (8), (11)...(13)
 <223> may be any amino acid

<400> 18

Phe Tyr Thr Xaa Ile Pro His Xaa Phe Gly Xaa Xaa Xaa Pro Pro
 1 5 10 15

<210> 19
 <211> 17
 <212> PRT

<213> artificial sequence

<220>

<223> part-sequence motif 5

<220>

<221> VARIANT

<222> (2)...(4), (6)...(7), (9), (13), (15)...(16)

<223> may be any amino acid

<400> 19

Lys Xaa Xaa Xaa Leu Xaa Xaa Leu Xaa Asp Ile Glu Xaa Ala Xaa Xaa
 1 5 10 15

Leu

<210> 20

<211> 11

<212> PRT

<213> artificial sequence

<220>

<223> part-sequence motif 6

<220>

<221> VARIANT

<222> (2)...(4), (6)

<223> may be any amino acid

<400> 20

Gly Xaa Xaa Xaa Leu Xaa Glu Val Ala Leu Gly
 1 5 10

<210> 21

<211> 28

<212> PRT

<213> artificial sequence

<220>

<223> part-sequence motif 7

<220>

<221> VARIANT

<222> (2)...(3), (5)...(8), (10)...(12), (14)...(22), (24), (26)...(27)

<223> may be any amino acid; residues 21 and 22 may be present or absent

<400> 21

Gly Xaa Xaa Ser Xaa Xaa Xaa Xaa Gly Xaa Xaa Xaa Pro Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Leu Xaa Gly Xaa Xaa Val
 20 25

<210> 22
 <211> 16
 <212> PRT
 <213> artificial sequence

<220>
 <223> part-sequence motif 8

<220>
 <221> VARIANT
 <222> (2)
 <223> Tyr or Phe

<220>
 <221> VARIANT
 <222> (3)...(4), (6)...(8), (10)...(13)
 <223> may be any amino acid

<400> 22

Glu	Xaa	Xaa	Xaa	Tyr	Xaa	Xaa	Xaa	Gln	Xaa	Xaa	Xaa	Xaa	Tyr	Leu	Leu
1				5				10						15	

<210> 23
 <211> 20
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic sequence for antibody production

<400> 23

Met	Ala	Ala	Arg	Arg	Arg	Arg	Ser	Thr	Gly	Gly	Gly	Arg	Ala	Arg	Ala
1				5					10					15	

Leu	Asn	Glu	Ser
			20

<210> 24
 <211> 20
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic sequence for antibody production

<400> 24

Lys	Thr	Glu	Leu	Gln	Ser	Pro	Glu	His	Pro	Leu	Asp	Gln	His	Tyr	Arg
1				5					10					15	

Asn	Leu	His	Cys
			20

<210> 25
 <211> 21
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic sequence for antibody production

<400> 25

Cys Lys Gly Arg Gln Ala Gly Arg Glu Glu Asp Pro Phe Arg Ser Thr
 1 5 10 15

Ala Glu Ala Leu Lys
 20

<210> 26
 <211> 20
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic sequence for antibody production

<400> 26

Cys Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu
 1 5 10 15

Glu Ala Leu Lys
 20

<210> 27
 <211> 19
 <212> PRT
 <213> artificial sequence

<220>
 <223> synthetic sequence for antibody production

<400> 27

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu
 1 5 10 15

Ala Leu Lys

<210> 28
 <211> 19
 <212> PRT
 <213> Mus musculus

<400> 28

Lys Gln Gln Ile Ala Arg Gly Phe Glu Ala Leu Glu Ala Leu Glu Glu
 1 5 10 15

Ala Met Lys

<210> 29
 <211> 7
 <212> PRT
 <213> artificial sequence

<220>
 <223> NAD+ binding domain

<220>
 <221> VARIANT
 <222> (2)...(4)
 <223> may be any amino acid residue

<400> 29

Gly Xaa Xaa Xaa Gly Lys Gly
 1 5

<210> 30
 <211> 38
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> PARP zinc finger sequence motif

<220>
 <221> VARIANT
 <222> (2)...(3), (5)...(34), (36)...(37)
 <223> may be any amino acid; residues 33 and 34 may be present or absent

<400> 30

Cys Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 20 25 30

Xaa Xaa His Xaa Xaa Cys
 35

<210> 31
 <211> 10
 <212> PRT
 <213> Arabidopsis thaliana

<400> 31

Ala Ala Val Leu Asp Gln Trp Ile Pro Asp
 1 5 10

<210> 32

<211> 39
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1)...(39)

<400> 32

gta tgc cag gaa ggt cat ggg cca gca aaa ggg tct ctg
 Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser
 1 5 10

39

<210> 33
 <211> 13
 <212> PRT
 <213> Homo sapiens

<400> 33

Gly Met Pro Gly Arg Ser Trp Ala Ser Lys Arg Val Ser
 1 5 10

<210> 34
 <211> 577
 <212> PRT
 <213> artificial sequence

<220>
 <223> sequence is hypothetical majority consensus sequence

<220>
 <221> VARIANT
 <222> 36, 48, 51 to 53, 57, 68, 72, 74, 80, 85, 89, 92, 106, 122,
 126, 147, 156, 160, 173, 177, 189, 191, 202, 205, 212, 226,
 242, 245, 275, 277, 280, 291, 302, 304, 313, 332, 336 to 338,
 340, 342, 370, 385, 393, 404, 467, 470, 475, 492, 493, 540,
 543, 545, 558, 575
 <223> may be any amino acid residue

<400> 34

Met Ala Gly Gly Leu Arg Pro Glu Arg Cys Glu Lys Gly Lys Arg Asp
 5 10 15

Lys Asp Lys Leu Leu Lys Val Phe Ala Glu Cys Tyr Cys Gly Ala Pro
 20 25 30

Lys Arg Lys Xaa Trp Val Gln Thr Glu Gly Ser Glu Lys Lys Lys Xaa
 35 40 45

Arg Gln Xaa Xaa Xaa Glu Glu Asp Xaa Phe Arg Ser Thr Ala Glu Ala
 50 55 60

Leu Lys Ala Xaa Pro Ala Glu Xaa Arg Xaa Ile Arg Val Asp Pro Xaa
 65 70 75 80

Cys	Pro	Leu	Ser	Xaa	Asn	Pro	Gly	Xaa	Gln	Val	Xaa	Glu	Asp	Val	Tyr		
				85					90					95			
Asp	Cys	Thr	Leu	Asn	Gln	Thr	Asn	Ile	Xaa	Asn	Asn	Asn	Asn	Lys	Phe		
			100					105						110			
Tyr	Ile	Ile	Gln	Leu	Leu	Glu	Asp	Asp	Xaa	Arg	Phe	Phe	Xaa	Cys	Trp		
			115				120					125					
Asn	Arg	Trp	Gly	Arg	Val	Gly	Glu	Val	Gly	Gln	Ser	Lys	Leu	Asn	His		
	130					135					140						
Phe	Thr	Xaa	Leu	Glu	Asp	Ala	Lys	Glu	Asp	Phe	Xaa	Lys	Lys	Phe	Xaa		
145					150					155					160		
Glu	Lys	Glu	Thr	Lys	Asn	Asn	Trp	Glu	Glu	Arg	Asp	Xaa	Phe	Val	Lys		
				165					170					175			
Xaa	Pro	Gly	Lys	Tyr	Thr	Leu	Leu	Glu	Val	Asp	Tyr	Xaa	Glu	Xaa	Glu		
			180					185					190				
Asp	Glu	Glu	Ala	Val	Val	Lys	Ser	Leu	Xaa	Val	Asp	Xaa	Gly	Pro	Val		
		195					200					205					
Ser	Thr	Val	Xaa	Lys	Arg	Val	Gln	Pro	Cys	Ser	Leu	Asp	Pro	Ala	Thr		
	210					215					220						
Gln	Xaa	Leu	Ile	Thr	Asn	Ile	Phe	Ser	Val	Glu	Met	Phe	Lys	Asn	Ala		
225					230					235					240		
Met	Xaa	Leu	Met	Xaa	Leu	Asp	Val	Lys	Lys	Met	Pro	Leu	Gly	Lys	Leu		
				245					250					255			
Ser	Lys	Gln	Gln	Ile	Ala	Ala	Gly	Phe	Glu	Ala	Leu	Glu	Ala	Leu	Glu		
			260					265					270				
Glu	Ala	Xaa	Lys	Xaa	Gly	Thr	Xaa	Gly	Gly	Gln	Ser	Leu	Glu	Glu	Leu		
		275					280					285					
Ser	Ser	Xaa	Phe	Tyr	Thr	Val	Ile	Pro	His	Asp	Phe	Gly	Xaa	Ser	Xaa		
	290					295					300						
Pro	Pro	Leu	Ile	Asn	Ser	Pro	Asp	Xaa	Leu	Gln	Ala	Lys	Lys	Asp	Met		
305				310						315					320		
Leu	Leu	Val	Leu	Ala	Asp	Ile	Glu	Leu	Ala	Gln	Xaa	Leu	Gln	Ala	Xaa		
				325					330					335			
Xaa	Xaa	Glu	Xaa	Ser	Xaa	Lys	Val	Glu	Glu	Val	Pro	His	Pro	Leu	Asp		
			340					345					350				
Arg	Asp	Tyr	Gln	Leu	Leu	Lys	Cys	Gln	Leu	Gln	Leu	Leu	Asp	Ser	Gly		
		355					360					365					
Ser	Xaa	Glu	Tyr	Lys	Val	Ile	Gln	Thr	Tyr	Leu	Lys	Gln	Thr	Gly	Ala		
	370					375					380						
Xaa	Thr	His	Cys	Pro	Tyr	Thr	Leu	Xaa	Asp	Ile	Phe	Lys	Val	Glu	Arg		
385					390					395					400		

Glu Gly Glu Xaa Asp Arg Phe Gln Ala His Ser Lys Leu Gly Asn Arg
 405 410 415
 Arg Leu Leu Trp His Gly Ser Asn Met Ala Val Val Ala Gly Ile Leu
 420 425 430
 Ser Ser Gly Leu Arg Ile Ala Pro His Glu Ala Pro Ser Gly Gly Arg
 435 440 445
 Val Gly Lys Gly Ile Tyr Phe Ala Ser Glu Asn Ser Lys Ser Ala Gly
 450 455 460
 Tyr Val Xaa Thr Ser Xaa Cys Gly Gly His Xaa Val Gly Leu Met Leu
 465 470 475 480
 Leu Gly Glu Val Ala Leu Gly Glu His Glu Leu Xaa Xaa Ala Asn Pro
 485 490 495
 Ser Leu Lys Ser Leu Pro Pro Gly Lys Asp Ser Val Ile Gly Leu Gly
 500 505 510
 Lys Thr Glu Pro Asp Pro Ala Gln Asp Ile Glu Leu Glu Leu Asp Gly
 515 520 525
 Gln Gly Val Val Val Pro Leu Gly Pro Pro Val Xaa Cys Gly Xaa Phe
 530 535 540
 Xaa Ser Ser Phe Ser Leu Tyr Ser Glu Tyr Leu Val Tyr Xaa Glu Ser
 545 550 555 560
 Gln Val Arg Leu Arg Tyr Leu Leu Glu Val His Phe Asn Phe Xaa Leu
 565 570 575

Trp

<210> 35
 <211> 1014
 <212> PRT
 <213> Homo sapiens

<400> 35

Met Ala Glu Ser Ser Asp Lys Leu Tyr Arg Val Glu Tyr Ala Lys Ser
 5 10 15
 Glu Arg Ala Ser Cys Lys Lys Cys Ser Glu Ser Ile Pro Lys Asp Ser
 20 25 30
 Leu Arg Met Ala Ile Met Val Gln Ser Pro Met Phe Asp Gly Lys Val
 35 40 45
 Pro His Trp Tyr His Phe Ser Cys Phe Trp Lys Val Gly His Ser Ile
 50 55 60
 Arg His Pro Asp Val Glu Val Asp Gly Phe Ser Glu Leu Arg Trp Asp
 65 70 75 80
 Asp Gln Gln Lys Val Lys Lys Thr Ala Glu Ala Gly Gly Val Thr Gly

				85					90					95			
Lys	Gly	Gln	Asp 100	Gly	Ile	Gly	Ser	Lys 105	Ala	Glu	Lys	Thr	Leu 110	Gly	Asp		
Phe	Ala	Ala 115	Glu	Tyr	Ala	Lys	Ser 120	Asn	Arg	Ser	Thr	Cys 125	Lys	Gly	Cys		
Met	Glu 130	Lys	Ile	Glu	Lys	Gly 135	Gln	Val	Arg	Leu	Ser 140	Lys	Lys	Met	Val		
Asp 145	Pro	Glu	Lys	Pro	Gln 150	Leu	Gly	Met	Ile	Asp 155	Arg	Trp	Tyr	His	Pro 160		
Gly	Cys	Phe	Val	Lys 165	Asn	Arg	Glu	Glu 170	Leu	Gly	Phe	Arg	Pro	Glu 175	Tyr		
Ser	Ala	Ser	Gln 180	Leu	Lys	Gly	Phe	Ser 185	Leu	Leu	Ala	Thr	Glu 190	Asp	Lys		
Glu	Ala	Leu 195	Lys	Lys	Gln	Leu	Pro 200	Gly	Val	Lys	Ser	Glu 205	Gly	Lys	Arg		
Lys	Gly 210	Asp	Lys	Val	Asp	Gly 215	Val	Asp	Glu	Val 220	Ala	Lys	Lys	Lys	Ser		
Lys 225	Lys	Glu	Lys	Asp	Lys 230	Asp	Ser	Lys	Leu	Glu 235	Lys	Ala	Leu	Lys	Ala 240		
Gln	Asn	Asp	Leu	Ile 245	Trp	Asn	Ile	Lys	Asp 250	Glu	Leu	Lys	Lys	Val 255	Cys		
Ser	Thr	Asn	Asp 260	Leu	Lys	Glu	Leu 265	Leu	Ile	Phe	Asn	Lys	Gln 270	Gln	Val		
Pro	Ser	Gly 275	Glu	Ser	Ala	Ile	Leu 280	Asp	Arg	Val	Ala	Asp 285	Gly	Met	Val		
Phe	Gly 290	Ala	Leu	Leu	Pro	Cys 295	Glu	Glu	Cys	Ser	Gly 300	Gln	Leu	Val	Phe		
Lys 305	Ser	Asp	Ala	Tyr	Tyr 310	Cys	Thr	Gly	Asp	Val 315	Thr	Ala	Trp	Thr	Lys 320		
Cys	Met	Val	Lys	Thr 325	Gln	Thr	Pro	Asn	Arg 330	Lys	Glu	Trp	Val	Thr 335	Pro		
Lys	Glu	Phe	Arg 340	Glu	Ile	Ser	Tyr	Leu 345	Lys	Lys	Leu	Lys	Val 350	Lys	Lys		
Gln	Asp	Arg 355	Ile	Phe	Pro	Pro	Glu 360	Thr	Ser	Ala	Ser	Val 365	Ala	Ala	Thr		
Pro	Pro 370	Pro	Ser	Thr	Ala	Ser 375	Ala	Pro	Ala	Ala	Val 380	Asn	Ser	Ser	Ala		
Ser 385	Ala	Asp	Lys	Pro	Leu 390	Ser	Asn	Met	Lys	Ile 395	Leu	Thr	Leu	Gly	Lys 400		

Leu Ser Arg Asn Lys Asp Glu Val Lys Ala Met Ile Glu Lys Leu Gly
 405 410 415
 Gly Lys Leu Thr Gly Thr Ala Asn Lys Ala Ser Leu Cys Ile Ser Thr
 420 425 430
 Lys Lys Glu Val Glu Lys Met Asn Lys Lys Met Glu Glu Val Lys Glu
 435 440 445
 Ala Asn Ile Arg Val Val Ser Glu Asp Phe Leu Gln Asp Tyr Ser Ala
 450 455 460
 Ser Thr Lys Ser Leu Gln Glu Leu Phe Leu Ala His Ile Leu Ser Pro
 465 470 475 480
 Trp Gly Ala Glu Val Lys Ala Glu Pro Val Glu Val Val Ala Pro Arg
 485 490 495
 Gly Lys Ser Gly Ala Ala Leu Ser Lys Lys Ser Lys Gly Gln Val Lys
 500 505 510
 Glu Glu Gly Ile Asn Lys Ser Glu Lys Arg Met Lys Leu Thr Leu Lys
 515 520 525
 Gly Gly Ala Ala Val Asp Pro Asp Ser Gly Leu Glu His Ser Ala His
 530 535 540
 Val Leu Glu Lys Gly Gly Lys Val Phe Ser Ala Thr Leu Gly Leu Val
 545 550 555 560
 Asp Ile Val Lys Gly Thr Asn Ser Tyr Tyr Lys Leu Gln Leu Leu Glu
 565 570 575
 Asp Asp Lys Glu Asn Arg Tyr Trp Ile Phe Arg Ser Trp Gly Arg Val
 580 585 590
 Gly Thr Val Ile Gly Ser Asn Lys Leu Glu Gln Met Pro Ser Lys Glu
 595 600 605
 Asp Ala Ile Glu His Pro Met Lys Leu Tyr Glu Glu Lys Thr Gly Asn
 610 615 620
 Ala Trp His Ser Lys Asn Phe Thr Lys Tyr Pro Lys Lys Pro Tyr Pro
 625 630 635 640
 Leu Glu Ile Asp Tyr Gly Gln Asp Glu Glu Ala Val Lys Lys Leu Thr
 645 650 655
 Val Asn Pro Gly Thr Lys Ser Lys Leu Pro Lys Pro Val Gln Asp Leu
 660 665 670
 Ile Lys Met Ile Pro Asp Val Glu Ser Met Lys Lys Ala Met Val Glu
 675 680 685
 Tyr Glu Ile Asp Leu Gln Lys Met Pro Leu Gly Lys Leu Ser Lys Arg
 690 695 700
 Gln Ile Gln Ala Ala Tyr Ser Ile Leu Ser Glu Val Gln Gln Ala Val
 705 710 715 720

Ser Gln Gly Ser Ser Asp Ser Gln Ile Leu Asp Leu Ser Asn Arg Phe
 725 730 735
 Tyr Thr Leu Ile Pro His Asp Phe Gly Met Lys Lys Pro Pro Leu Leu
 740 745 750
 Asn Asn Ala Asp Ser Val Gln Ala Lys Val Glu Met Leu Asp Asn Leu
 755 760 765
 Leu Asp Ile Glu Val Ala Tyr Ser Leu Leu Arg Gly Gly Ser Asp Asp
 770 775 780
 Ser Ser Lys Asp Pro Ile Asp Val Asn Tyr Glu Lys Leu Lys Thr Asp
 785 790 795 800
 Ile Lys Val Val Asp Arg Asp Ser Glu Glu Ala Glu Ile Ile Arg Lys
 805 810 815
 Tyr Val Lys Asn Thr His Ala Thr Thr His Asn Ala Tyr Asp Leu Glu
 820 825 830
 Val Ile Asp Ile Phe Lys Ile Glu Arg Glu Gly Glu Cys Gln Arg Tyr
 835 840 845
 Lys Pro Pro Lys Gln Leu His Asn Arg Arg Leu Leu Trp His Gly Ser
 850 855 860
 Arg Thr Thr Asn Phe Ala Gly Ile Leu Ser Gln Gly Leu Arg Ile Ala
 865 870 875 880
 Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly Ile Tyr
 885 890 895
 Phe Ala Asp Met Val Ser Lys Ser Ala Asn Tyr Cys His Thr Ser Gln
 900 905 910
 Gly Asp Pro Ile Gly Leu Ile Leu Leu Gly Glu Val Ala Leu Gly Asn
 915 920 925
 Met Tyr Glu Leu Lys His Ala Ser His Ile Ser Lys Leu Pro Lys Gly
 930 935 940
 Lys His Ser Val Lys Gly Leu Gly Lys Thr Thr Pro Asp Pro Ser Ala
 945 950 955 960
 Asn Ile Ser Leu Asp Gly Val Asp Val Pro Leu Gly Thr Gly Ile Ser
 965 970 975
 Ser Gly Val Asn Asp Thr Ser Leu Leu Tyr Asn Glu Tyr Ile Val Tyr
 980 985 990
 Asp Ile Ala Gln Val Asn Leu Lys Tyr Leu Leu Lys Leu Lys Phe Asn
 995 1000 1005
 Phe Lys Thr Ser Leu Trp
 1010
